

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Glimcher, Laurie H. et al.

10 (ii) TITLE OF INVENTION: Human c-Maf Compositions and
Methods of Use Thereof

10 (iii) NUMBER OF SEQUENCES: 2

15 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
(B) STREET: 28 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
30 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/030,579
(B) FILING DATE: 2-FEB-1998

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kara, Catherine J.
(B) REGISTRATION NUMBER: 41,106
(C) REFERENCE/DOCKET NUMBER: HUI-027CP

40 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)227-7400
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(2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1203

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCA TCA GAA CTG GCA ATG AGC AAC TCC GAC CTG CCC ACC AGT CCC
48
Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
10 1 5 10 15
CTG GCC ATG GAA TAT GTT AAT GAC TTC GAT CTG ATG AAG TTT GAA GTG
96
Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
15 20 25 30
AAA AAG GAA CCG GTG GAG ACC GAC CGC ATC ATC AGC CAG TGC GGC CGT
144
Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
20 35 40 45
CTC ATC GCC GGG GGC TCG CTG TCC TCC ACC CCC ATG AGC ACG CCC TGC
192
Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
25 50 55 60
AGC TCG GTG CCC CCG TCC CCC AGC TTC TCG GCG CCC AGC CCG GGC TCG
240
Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
30 65 70 75 80
CGA GGC GAA CAG AAG GCG CAC CTG GAA GAC TAC TAC TGG ATG ACC GGC
288
Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
35 85 90 95
TAC CCG CAG CAG CTG AAC CCC GAG GCG CTG GGC TTC AGC CCC GAG GAC
336
Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
40 100 105 110
GCG GTC GAG GCG CTC ATC AGC AAC AGC CAC CAG CTC CGG GGC GGC TTC
384
Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
45 115 120 125
GAT GGC TAT GCG CGC GGG GCG CAG CAG CTA GCC GCG GCG GCC GGG GCA
432
Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Gly Ala
50 130 135 140
GGT GCC GGC GCC TCC TTG GGC GGC AGC GGC GAG GAG ATG GGC CCC GCC
480
Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
55 145 150 155 160

GCC GCC GTG GTG TCC GCC GTG ATC GCC GCG GCC GCC GCG CAG AGC GGC
528
Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Gln Ser Gly
165 170 175
5
GCG GGC CCG CAC TAC CAC CAC CAC CAC CAC GGC GCC GGC CAC CAC
576
Ala Gly Pro His Tyr His His His His Ala Ala Gly His His
180 185 190
10
CAC CAC CCG ACG GCC GGC GCG CCC GGC GCC GCG GGC AGC GCG GCC GCT
624
His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala
195 200 205
15
TCG GCC GGT GGC GCT GGG GGC GCG GGC GGC GGT GGC CCG GCC AGC GTT
672
Ser Ala Gly Gly Ala Gly Gly Gly Gly Gly Pro Ala Ser Val
210 215 220
20
GGG GGC GGC GGC GGC GGC GGC GGC GGA GGC GGC GGG GGC GCG GCG
720
Gly Ala Ala
225 230 235 240
25
GGC GCC CTG CAC CCG CAC CAC GCC GGC GGC CTG CAC TTC GAC GAC
768
Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
245 250 255
30
CGC TTC TCC GAC GAG CAG CTG GTG ACC ATG TCT GTG CGC GAC TGG AAC
816
Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
260 265 270
35
CGG CAG CTG CGC GGG GTC AGC AAG GAG GAG GTG ATC CGG CTG AAG CAG
864
Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
275 280 285
40
AAG AGG CGG ACC CTG AAA AAC CGC GGC TAT GCC AAG TCC TGC CGC TTC
912
Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
290 295 300
45
AAG AGG GTG CAG CAG AGA CAC GTC CTG GAG TCG GAG AAG AAC CAG CTG
960
Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
305 310 315 320
50
CTG CAG CAA GTC GAC CAC CTC AAG CAG GAG ATC TCC AGG CTG GTG CGC
1008
Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
325 330 335
55
GAG AGG GAC GCG TAC AAG GAG AAA TAC GAG AAG TTG GTG AGC AGC GGC
1056

Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
340 345 350

5 TTC CGA GAA AAC GGC TCG AGC AGC GAC AAC CCG TCC TCT CCC GAG TTT
1104

Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
355 360 365

10 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC
1152

Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
370 375 380

15 ACA TTT TGG AAG CCC CAG CAT CGT GTA CTT ACC AGT GTG TTC ACA AAA
1200

Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
385 390 395 400

20 TGA
1203

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 amino acids
(B) TYPE: amino acid
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
1 5 10 15

40 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
20 25 30

Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
35 40 45

45 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
50 55 60

Ser Ser Val Pro Pro Ser Pro Phe Ser Ala Pro Ser Pro Gly Ser
65 70 75 80

55 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
85 90 95

Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
55 100 105 110

Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Phe

	115	120	125
	Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala		
	130	135	140
5	Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala		
	145	150	155
	160		
10	Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Gln Ser Gly		
	165	170	175
	Ala Gly Pro His Tyr His His His His Ala Ala Gly His His His		
	180	185	190
15	His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala		
	195	200	205
	Ser Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val		
	210	215	220
20	Gly Ala Ala		
	225	230	235
	240		
25	Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp		
	245	250	255
	Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn		
	260	265	270
30	Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln		
	275	280	285
	Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe		
	290	295	300
35	Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu		
	305	310	315
	320		
40	Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg		
	325	330	335
	Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly		
	340	345	350
45	Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe		
	355	360	365
	Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala		
	370	375	380
50	Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys		
	385	390	395
	400		